

SEQUENCE LISTING

<110> Sharpe, Arlene H.
 Borriello, Francescopaulo
 Freeman, Gordon J.
 Nadler, Lee M.

<120> B7 Domain-Specific Antibodies

<130> BWI-120CPADV2

<140> 09/837,867

<141> 2001-04-17

<150> 08/205,697

<151> 1994-03-02

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ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
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aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
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ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
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Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
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gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa				674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	130	135	140	
gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca				722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	145	150	155	
gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct				770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	160	165	170	
cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg				818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	175	180	185	190
aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa				866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	195	200	205	
cta gat ttc aat acg act cgc aac cac acc att aag tgt ctc att aaa				914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	210	215	220	
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Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	225	230	235	
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Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	240	245	250	
ttc ggc gca gta ata aca gtc gtc gtc atc gtt gtc atc atc aaa tgc				1058
Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	255	260	265	270
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Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala	275	280	285	
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Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser	290	295	300	
cta ggt gaa gcc tct gca gtg att tgc aga agt act cag acg aat gaa				1202
Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu	305	310	315	
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Pro Gln	320			
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<213> Mus musculus

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Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
          35          40          45
Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
          50          55          60
Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
65          70          75          80
Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
          85          90          95
Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
          100          105          110
Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
          115          120          125
Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
          130          135          140
Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
145          150          155          160
Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
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Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
          180          185          190
Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
          195          200          205
Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
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Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225          230          235          240
Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
          245          250          255
Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
          260          265          270
Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp
          275          280          285
Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly
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 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg aat cgt 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Asn Arg
 15 20 25 30

ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 35 40 45

aaa gat aag gta ttg ctg cct tgc cgt tac aac tct cct cat gaa gat 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 50 55 60

gag tct gaa gac cga atc tac tgg caa aaa cat gac aaa gtg gtg ctg 482
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 65 70 75

tct gtc att gct ggg aaa cta aaa gtg tgg ccc gag tat aag aac cgg 530
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 80 85 90

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 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 95 100 105 110

ctt tca gac cgg ggc aca tac agc tgt gtc gtt caa aag aag gaa aga 626
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 115 120 125

gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa 674
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 130 135 140

gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca 722
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gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct 770
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cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg 818
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 175 180 185 190

aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa 866
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
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cta gat ttc aat acg act cgc aac cac acc att aag tgt ctc att aaa	914
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Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	
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Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	
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Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala
20 25 30

tct gca gtg att tgc aga agt act cag acg aat gaa cca cag 138
Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

tagttctgct gtttctgagg acgtagttta gagactgaat tcttttgaaa ggacataggg 198
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35 40 45

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<213> Mus musculus

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<213> Mus musculus

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<222> (249)...(848)

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        1             5             10

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aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
  15             20             25             30

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ctt tca caa gtg tct tca gct gac ttc tct acc ccc aac ata act gag 386
Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
             35             40             45

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Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu
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tta cct ggc atc aat acg aca att tcc cag gat cct gaa tct gaa ttg 530

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 80                               85                               90

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Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr
 95                               100                               105                               110

att aag tgt ctc att aaa tat gga gat gct cac gtg tca gag gac ttc 626
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 115                               120                               125

acc tgg gaa aaa ccc cca gaa gac cct cct gat agc aag aac aca ctt 674
Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu
 130                               135                               140

gtg ctc ttt ggg gca gga ttc ggc gca gta ata aca gtc gtc gtc atc 722
Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile
 145                               150                               155

gtt gtc atc atc aaa tgc ttc tgt aag cac aga agc tgt ttc aga aga 770
Val Val Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg
 160                               165                               170

aat gag gca agc aga gaa aca aac aac agc ctt acc ttc ggg cct gaa 818
Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu
 175                               180                               185                               190

gaa gca tta gct gaa cag acc gtc ttc ctt tagttcttct ctgtccatgt 868
Glu Ala Leu Ala Glu Gln Thr Val Phe Leu
 195                               200

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gatttctttc catcaggaag ctacgggcaa gtttgctggg cctttgattg cttgatgact 1048
gaagtggaaa ggctgagccc actgtgggtg gtgctagccc tgggcagggg cagggtgaccc 1108
tggttggtat aagaaaaaga gctgtcacta aaaggagagg tgcctagtct tactgcaact 1168
tgatatgtca tgtttggttg gtgtctgttg gaggcctgcc cttttctgaa gagaagtggg 1228
gggagagtgg atgggggtggg ggcagaggaa aagtggggga gagggcctgg gaggagagga 1288
gggaggggga cggggtgggg gtgggggaaa ctatggttgg gatgtaaaaa cggataataa 1348
tataaatatt aaataaaaag agagtattga gcaaaaaaaa aaaaaaaaaa 1398

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<210> 9

<211> 200

<212> PRT

<213> Mus musculus

<400> 9

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Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20           25           30
Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35           40           45
Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50           55           60
Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65           70           75           80
Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85           90           95
Ile Ser Ser Gln Leu Asp Phe Asn Thr Arg Asn His Thr Ile Lys
 100          105          110

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Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp
		115					120					125			
Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu
	130					135					140				
Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val
145					150					155					160
Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu
			165						170					175	
Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala
			180					185					190		
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		195					200								

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 tggatgccat ccaggcttct tttctacat ctctgtttct cgatttttgt gagcctagga 180
 ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
 ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30

ctt tca caa gtg tct tca gct gac ttc tct acc ccc aac ata act gag 386
 Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
 35 40 45

tct gga aac cca tct gca gac act aaa agg att acc tgc ttt gct tcc 434
 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser
 50 55 60

ggg ggt ttc cca aag cct cgc ttc tct tgg ttg gaa aat gga aga gaa 482
 Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu
 65 70 75

tta cct ggc atc aat acg aca att tcc cag gat cct gaa tct gaa ttg 530
 Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu
 80 85 90

tac acc att agt agc caa cta gat ttc aat acg act cgc aac cac acc 578
 Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr
 95 100 105 110

att aag tgt ctc att aaa tat gga gat gct cac gtg tca gag gac ttc 626
 Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe
 115 120 125

acc tgg gaa aaa ccc cca gaa gac cct cct gat agc aag aac aca ctt 674

Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	
			130					135					140			
gtg	ctc	ttt	ggg	gca	gga	ttc	ggc	gca	gta	ata	aca	gtc	gtc	gtc	atc	722
Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	
		145					150					155				
ggt	gtc	atc	atc	aaa	tgc	ttc	tgt	aag	cac	ggt	ctc	atc	tac	cat	ttg	770
Val	Val	Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Gly	Leu	Ile	Tyr	His	Leu	
	160					165					170					
caa	ctg	acc	tct	tct	gca	aag	gac	ttc	aga	aac	cta	gca	cta	ccc	tg	818
Gln	Leu	Thr	Ser	Ser	Ala	Lys	Asp	Phe	Arg	Asn	Leu	Ala	Leu	Pro	Trp	
175					180					185					190	
ctc	tgc	aaa	cac	ggt	tct	cta	ggt	gaa	gcc	tct	gca	gtg	att	tgc	aga	866
Leu	Cys	Lys	His	Gly	Ser	Leu	Gly	Glu	Ala	Ser	Ala	Val	Ile	Cys	Arg	
			195					200						205		
agt	act	cag	acg	aat	gaa	cca	cag	tagttctgct	gtttctgagg	acgtagttta						920
Ser	Thr	Gln	Thr	Asn	Glu	Pro	Gln									
			210													
gagactgaat	tcttttgaaa	ggacataggg	acagtttgca	catttgcttg	cacatcacac											980
acacacacac	acacacacac	acacacacac	acacacacac	acacacacac	acacacacac											1040
tctctctctc	tctctctctc	gataccttag	gatagggttc	taccctgttg	ctcagtgaca											1100
aagaatcact	ctgtggcgga	ggcaggcttc	aagcttgcag	caatcctcct	gcaccagttt											1160
cctgagtgcc	agacttccag	gtgtaagcta	tggcacttag	cagaacacta	gctgaatcaa											1220
tgaagacact	gaggttccaa	gagggaaacct	gaattatgaa	ggtgagtcag	aatccagatt											1280
tcttggtctc	accactctta	acctgtatct	gtagacccc	aagctctgag	ctcatagaca											1340
agctaattta	aaatgctttt	taataagcag	aaggctcagt	tagtacgggg	ttcaggatac											1400
tgcttactgg	caatatttga	ctagcctcta	ttttgtttgt	tttttaaagg	cctactgact											1460
gtagtgaat	ttgtaggaaa	catgttgcta	tgtataccca	tttgagggta	ataaaaatgt											1520
tggttaatttt	cagccagcac	tttcaggta	tttcctttt	tatccttcat												1570

<210> 11
 <211> 214
 <212> PRT
 <213> Mus musculus

<400> 11
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 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35 40 45
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50 55 60
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65 70 75 80
 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85 90 95
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys
 100 105 110
 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp
 115 120 125
 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu
 130 135 140
 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val
 145 150 155 160

Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu
 165 170 175
 Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys
 180 185 190
 Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr
 195 200 205
 Gln Thr Asn Glu Pro Gln
 210

<210> 12
 <211> 1261
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (194)...(1135)

<221> misc_feature
 <222> 3, 7
 <223> n = A,T,C or G

<400> 12
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 gctcctttta cttttcttct tttttatatt tttttacctt ctattttttt cttcatgttc 120
 ctgtgatctt cgggaatgct gctgtgcttg tgtgtgtggt ccctgagcgc cgaggtggag 180
 aggcactggg gac atg tat gtc atc aag aca tgt gca acc tgc acc atg 229
 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met
 1 5 10
 ggc ttg gca atc ctt atc ttt gtg aca gtc ttg ctg atc tca gat gct 277
 Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala
 15 20 25
 gtt tcc gtg gag acg caa gct tat ttc aat ggg act gca tat ctg ccg 325
 Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro
 30 35 40
 tgc cca ttt aca aag gct caa aac ata agc ctg agt gag ctg gta gta 373
 Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val
 45 50 55 60
 ttt tgg cag gac cag caa aag ttg gtt ctg tac gag cac tat ttg ggc 421
 Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly
 65 70 75
 aca gag aaa ctt gat agt gtg aat gcc aag tac ctg ggc cgc acg agc 469
 Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser
 80 85 90
 ttt gac agg aac aac tgg act cta cga ctt cac aat gtt cag atc aag 517
 Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys
 95 100 105
 gac atg ggc tcg tat gat tgt ttt ata caa aaa aag cca ccc aca gga 565
 Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly
 110 115 120
 tca att atc ctc caa cag aca tta aca gaa ctg tca gtg atc gcc aac 613
 Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn

125	130	135	140	
ttc agt gaa cct gaa ata aaa ctg gct cag aat gta aca gga aat tct				661
Phe Ser Glu Pro	Glu Ile Lys Leu	Ala Gln Asn Val	Thr Gly Asn Ser	
	145	150	155	
ggc ata aat ttg acc tgc acg tct aag caa ggt cac ccg aaa cct aag				709
Gly Ile Asn Leu	Thr Cys Thr Ser	Lys Gln Gly His	Pro Lys Pro Lys	
	160	165	170	
aag atg tat ttt ctg ata act aat tca act aat gag tat ggt gat aac				757
Lys Met Tyr Phe	Leu Ile Thr Asn	Ser Thr Asn Glu	Tyr Gly Asp Asn	
	175	180	185	
atg cag ata tca caa gat aat gtc aca gaa ctg ttc agt atc tcc aac				805
Met Gln Ile Ser	Gln Asp Asn Val	Thr Glu Leu Phe	Ser Ile Ser Asn	
	190	195	200	
agc ctc tct ctt tca ttc ccg gat ggt gtg tgg cat atg acc gtt gtg				853
Ser Leu Ser Leu	Ser Phe Pro Asp	Gly Val Trp His	Met Thr Val Val	
	210	215	220	
tgt gtt ctg gaa acg gag tca atg aag att tcc tcc aaa cct ctc aat				901
Cys Val Leu Glu	Thr Glu Ser Met	Lys Ile Ser Ser	Lys Pro Leu Asn	
	225	230	235	
ttc act caa gag ttt cca tct cct caa acg tat tgg aag gag att aca				949
Phe Thr Gln Glu	Phe Pro Ser Pro	Gln Thr Tyr Trp	Lys Glu Ile Thr	
	240	245	250	
gct tca gtt act gtg gcc ctc ctc ctt gtg atg ctg ctc atc att gta				997
Ala Ser Val Thr	Val Ala Leu Leu	Val Met Leu Leu	Ile Ile Val	
	255	260	265	
tgt cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc tct				1045
Cys His Lys Lys	Pro Asn Gln Pro	Ser Arg Pro Ser	Asn Thr Ala Ser	
	270	275	280	
aag tta gag cgg gat agt aac gct gac aga gag act atc aac ctg aag				1093
Lys Leu Glu Arg	Asp Ser Asn Ala	Asp Arg Glu Thr	Ile Asn Leu Lys	
	285	290	300	
gaa ctt gaa ccc caa att gct tca gca aaa cca aat gca gag				1135
Glu Leu Glu Pro	Gln Ile Ala Ser	Ala Lys Pro Asn	Ala Glu	
	305	310		
tgaaggcagt gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc				1195
agagttttctc agaattcaaaa aatgtttctca gctgattgga attctacagt tgaataatta				1255
aagaac				1261

<210> 13

<211> 314

<212> PRT

<213> Mus musculus

<400> 13

Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met Gly Leu Ala Ile

1

5

10

15

Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu

20

25

30

Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr

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<220>
<221> CDS
<222> (194)...(223)

<221> misc_feature
<222> 3, 7
<223> n = A,T,C or G
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$\langle 210 \rangle$	15
$\langle 211 \rangle$	10

<212> PRT

<213> Mus musculus

<400> 15

Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
1 5 10

<210> 16

<211> 1716

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(1166)

<400> 16

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tggatgccat ccaggcttct ttttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggttttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
1 5 10

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
15 20 25 30

ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
35 40 45

aaa gat aag gta ttg ctg cct tgc cgt tac aac tct cct cat gaa gat 434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
50 55 60

gag tct gaa gac cga atc tac tgg caa aaa cat gac aaa gtg gtg ctg 482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
65 70 75

tct gtc att gct ggg aaa cta aaa gtg tgg ccc gag tat aag aac cgg 530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
80 85 90

act tta tat gac aac act acc tac tct ctt atc atc ctg ggc ctg gtc 578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
95 100 105 110

ctt tca gac cgg ggc aca tac agc tgt gtc gtt caa aag aag gaa aga 626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
115 120 125

gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa 674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
130 135 140

gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca 722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
145 150 155

gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct 770
 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
 160 165 170

cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg 818
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
 175 180 185 190

aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa 866
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
 195 200 205

cta gat ttc aat acg act cgc aac cac acc att aag tgt ctc att aaa 914
 Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
 210 215 220

tat gga gat gct cac gtg tca gag gac ttc acc tgg gaa aaa ccc cca 962
 Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
 225 230 235

gaa gac cct cct gat agc aag aac aca ctt gtg ctc ttt ggg gca gga 1010
 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
 240 245 250

ttc ggc gca gta ata aca gtc gtc gtc atc gtt gtc atc atc aaa tgc 1058
 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
 255 260 265 270

ttc tgt aag cac aga agc tgt ttc aga aga aat gag gca agc aga gaa 1106
 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
 275 280 285

aca aac aac agc ctt acc ttc ggg cct gaa gaa gca tta gct gaa cag 1154
 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
 290 295 300

acc gtc ttc ctt tagttcttct ctgtccatgt gggatacatg gtattatgtg 1206
 Thr Val Phe Leu
 305

gctcatgagg tacaatcttt ctttcagcac cgtgctagct gatctttcgg acaacttgac 1266
 acaagataga gttaactggg aagagaaagc cttgaatgag gatttctttc catcaggaag 1326
 ctacgggcaa gtttgctggg cctttgattg cttgatgact gaagtggaaa ggctgagccc 1386
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 gctgtcacta aaaggagagg tgcctagtct tactgcaact tgatatgtca tgtttggttg 1506
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 agagtattga gcaaaaaaaaa aaaaaaaaaa 1716

<210> 17
 <211> 306
 <212> PRT
 <213> Mus musculus

<400> 17
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 20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110
 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 130 135 140
 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 145 150 155 160
 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 165 170 175
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 180 185 190
 Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
 195 200 205
 Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
 210 215 220
 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
 225 230 235 240
 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
 245 250 255
 Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
 260 265 270
 Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
 275 280 285
 Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
 290 295 300
 Phe Leu
 305

<210> 18
 <211> 1491
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (318)...(1181)

<400> 18
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 gtgaaactaa atccacaacc tttggagacc caggaacacc ctccaatctc tgtgtgtttt 180
 gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcagc cctgcctggt 240
 ttgcacctgg gaagtgcctt ggtcttactt gggtccaaat tgttggtttt cacttttgac 300
 cctaagcatc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 tcc aag tgt cca tac ctg aat ttc ttt cag ctc ttg gtg ctg gct ggt 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25

ctt tct cac ttc tgt tca ggt gtt atc cac gtg acc aag gaa gtg aaa	446
Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys	
30 35 40	
gaa gtg gca acg ctg tcc tgt ggt cac aat gtt tct gtt gaa gag ctg	494
Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu	
45 50 55	
gca caa act cgc atc tac tgg caa aag gag aag aaa atg gtg ctg act	542
Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr	
60 65 70 75	
atg atg tct ggg gac atg aat ata tgg ccc gag tac aag aac cgg acc	590
Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr	
80 85 90	
atc ttt gat atc act aat aac ctc tcc att gtg atc ctg gct ctg cgc	638
Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg	
95 100 105	
cca tct gac gag ggc aca tac gag tgt gtt gtt ctg aag tat gaa aaa	686
Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys	
110 115 120	
gac gct ttc aag cgg gaa cac ctg gct gaa gtg acg tta tca gtc aaa	734
Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys	
125 130 135	
gct gac ttc cct aca cct agt ata tct gac ttt gaa att cca act tct	782
Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser	
140 145 150 155	
aat att aga agg ata att tgc tca acc tct gga ggt ttt cca gag cct	830
Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro	
160 165 170	
cac ctc tcc tgg ttg gaa aat gga gaa gaa tta aat gcc atc aac aca	878
His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr	
175 180 185	
aca gtt tcc caa gat cct gaa act gag ctc tat gct gtt agc agc aaa	926
Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys	
190 195 200	
ctg gat ttc aat atg aca acc aac cac agc ttc atg tgt ctc atc aag	974
Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys	
205 210 215	
tat gga cat tta aga gtg aat cag acc ttc aac tgg aat aca acc aag	1022
Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys	
220 225 230 235	
caa gag cat ttt cct gat aac ctg ctc cca tcc tgg gcc att acc tta	1070
Gln Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu	
240 245 250	
atc tca gta aat gga att ttt gtg ata tgc tgc ctg acc tac tgc ttt	1118
Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe	
255 260 265	
gcc cca aga tgc aga gag aga agg agg aat gag aga ttg aga agg gaa	1166

Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu
270 275 280

agt gta cgc cct gta taacagtgtc cgcagaagca aggggctgaa aagatctgaa 1221
Ser Val Arg Pro Val
285

ggtagcctcc gtcattctctt ctgggataca tggatcgtgg ggatcatgag gcattcttcc 1281
cttaacaaat ttaagctgtt ttaccacta cctcaccttc ttaaaaacct ctttcagatt 1341
aagctgaaca gttacaagat ggctggcatc cctctccttt ctcccatat gcaatttgct 1401
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aattcattat ctattaaaca ctaatttgag 1491

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<211> 288
<212> PRT
<213> Homo sapiens

<400> 19
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Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190
Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205
Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220
Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240
Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255
Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270
Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

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<211> 1151
<212> DNA
<213> Mus musculus

<220>

<221> CDS

<222> (99) ... (1025)

<400> 20

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cctgtagacg tgttccagaa cttacggaag caccacacg atg gac ccc aga tgc acc 116
Met Asp Pro Arg Cys Thr
1 5

atg ggc ttg gca atc ctt atc ttt gtg aca gtc ttg ctg atc tca gat 164
Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp
10 15 20

gct gtt tcc gtg gag acg caa gct tat ttc aat ggg act gca tat ctg 212
Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu
25 30 35

ccg tgc cca ttt aca aag gct caa aac ata agc ctg agt gag ctg gta 260
Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val
40 45 50

gta ttt tgg cag gac cag caa aag ttg gtt ctg tac gag cac tat ttg 308
Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu
55 60 65 70

ggc aca gag aaa ctt gat agt gtg aat gcc aag tac ctg ggc cgc acg 356
Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr
75 80 85

agc ttt gac agg aac aac tgg act cta cga ctt cac aat gtt cag atc 404
Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile
90 95 100

aag gac atg ggc tgc tat gat tgt ttt ata caa aaa aag cca ccc aca 452
Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr
105 110 115

gga tca att atc ctc caa cag aca tta aca gaa ctg tca gtg atc gcc 500
Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala
120 125 130

aac ttc agt gaa cct gaa ata aaa ctg gct cag aat gta aca gga aat 548
Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn
135 140 145 150

tct ggc ata aat ttg acc tgc acg tct aag caa ggt cac ccg aaa cct 596
Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro
155 160 165

aag aag atg tat ttt ctg ata act aat tca act aat gag tat ggt gat 644
Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp
170 175 180

aac atg cag ata tca caa gat aat gtc aca gaa ctg ttc agt atc tcc 692
Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser
185 190 195

aac agc ctc tct ctt tca ttc ccg gat ggt gtg tgg cat atg acc gtt 740
Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val

200	205	210	
gtg tgt gtt ctg gaa acg gag tca atg aag att tcc tcc aaa cct ctc			788
Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu			
215	220	225	230
aat ttc act caa gag ttt cca tct cct caa acg tat tgg aag gag att			836
Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile			
235	240		245
aca gct tca gtt act gtg gcc ctc ctc ctt gtg atg ctg ctc atc att			884
Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile			
250	255		260
gta tgt cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc			932
Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala			
265	270		275
tct aag tta gag cgg gat agt aac gct gac aga gag act atc aac ctg			980
Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu			
280	285		290
aag gaa ctt gaa ccc caa att gct tca gca aaa cca aat gca gag			1025
Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu			
295	300	305	
tgaaggcagt gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc			1085
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aagaac			1151

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 <213> Mus musculus

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 Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
 35 40 45
 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
 50 55 60
 Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
 65 70 75 80
 Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
 85 90 95
 Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
 100 105 110
 Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
 115 120 125
 Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
 130 135 140
 Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
 145 150 155 160
 Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
 165 170 175
 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
 180 185 190
 Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly

195	200	205
Val Trp His Met Thr	Val Val Cys Val Leu Glu Thr	Glu Ser Met Lys
210	215	220
Ile Ser Ser Lys Pro	Leu Asn Phe Thr Gln Glu Phe	Pro Ser Pro Gln
225	230	235
Thr Tyr Trp Lys Glu	Ile Thr Ala Ser Val Thr Val	Ala Leu Leu Leu
245	250	255
Val Met Leu Leu Ile	Ile Val Cys His Lys Lys	Pro Asn Gln Pro Ser
260	265	270
Arg Pro Ser Asn Thr	Ala Ser Lys Leu Glu Arg	Asp Ser Asn Ala Asp
275	280	285
Arg Glu Thr Ile Asn	Leu Lys Glu Leu Glu	Pro Gln Ile Ala Ser Ala
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Lys Pro Asn Ala Glu		
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 Met Asp Pro
 1

cag tgc act atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg 163
 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
 5 10 15

ctc tct ggt gct gct cct ctg aag att caa gct tat ttc aat gag act 211
 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
 20 25 30 35

gca gac ctg cca tgc caa ttt gca aac tct caa aac caa agc ctg agt 259
 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
 40 45 50

gag cta gta gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag 307
 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
 55 60 65

gta tac tta ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg 355
 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
 70 75 80

ggc cgc aca agt ttt gat tgc gac agt tgg acc ctg aga ctt cac aat 403
 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
 85 90 95

ctt cag atc aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa 451
 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
 100 105 110 115

aag ccc aca gga atg att cgc atc cac cag atg aat tct gaa ctg tca 499

Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser		
				120					125					130			
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Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile		
			135					140					145				
aca	gaa	aat	gtg	tac	ata	aat	ttg	acc	tgc	tca	tct	ata	cac	ggg	tac	595	
Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr		
		150					155					160					
cca	gaa	cct	aag	aag	atg	agt	gtt	ttg	cta	aga	acc	aag	aat	tca	act	643	
Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr		
	165					170					175						
atc	gag	tat	gat	ggg	att	atg	cag	aaa	tct	caa	gat	aat	gtc	aca	gaa	691	
Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu		
180					185					190					195		
ctg	tac	gac	gtt	tcc	atc	agc	ttg	tct	gtt	tca	ttc	cct	gat	gtt	acg	739	
Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr		
				200					205					210			
agc	aat	atg	acc	atc	ttc	tgt	att	ctg	gaa	act	gac	aag	acg	cgg	ctt	787	
Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu		
			215					220					225				
tta	tct	tca	cct	ttc	tct	ata	gag	ctt	gag	gac	cct	cag	cct	ccc	cca	835	
Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro		
			230				235					240					
gac	cac	att	cct	tgg	att	aca	gct	gta	ctt	cca	aca	gtt	att	ata	tgt	883	
Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys		
	245					250					255						
gtg	atg	gtt	ttc	tgt	cta	att	cta	tgg	aaa	tgg	aag	aag	aag	aag	cgg	931	
Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg		
260					265				270						275		
cct	cgc	aac	tct	tat	aaa	tgt	gga	acc	aac	aca	atg	gag	agg	gaa	gag	979	
Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu		
				280					285					290			
agt	gaa	cag	acc	aag	aaa	aga	gaa	aaa	atc	cat	ata	cct	gaa	aga	tct	1027	
Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser		
			295					300					305				
gat	gaa	gcc	cag	cgt	gtt	ttt	aaa	agt	tcg	aag	aca	tct	tca	tgc	gac	1075	
Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp		
		310					315					320					
aaa	agt	gat	aca	tgt	ttt	taattaaaga	gtaaagccca	aaaaaaaa								1120	
Lys	Ser	Asp	Thr	Cys	Phe												
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<210> 23
 <211> 329
 <212> PRT
 <213> Homo sapiens

<400> 23

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20      25      30
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35      40      45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50      55      60
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65      70      75      80
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85      90      95
Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100     105     110
His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115     120     125
Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130     135     140
Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145     150     155     160
His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165     170     175
Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180     185     190
Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195     200     205
Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210     215     220
Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225     230     235     240
Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245     250     255
Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260     265     270
Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275     280     285
Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290     295     300
Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305     310     315     320
Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

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<210> 24

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148)...(1134)

<400> 24

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cagtggacag gcatttgtga cagcact atg gat ccc cag tgc act atg gga ctg 174
Met Asp Pro Gln Cys Thr Met Gly Leu
1      5

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agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt gct gct cct	222
Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala Pro	
10 15 20 25	
ctg aag att caa gct tat ttc aat gag act gca gac ctg cca tgc caa	270
Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys Gln	
30 35 40	
ttt gca aac tct caa aac caa agc ctg agt gag cta gta gta ttt tgg	318
Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val Phe Trp	
45 50 55	
cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta ggc aaa gag	366
Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly Lys Glu	
60 65 70	
aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca agt ttt gat	414
Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser Phe Asp	
75 80 85	
tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc aag gac aag	462
Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys Asp Lys	
90 95 100 105	
ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca gga atg att	510
Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly Met Ile	
110 115 120	
cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct aac ttc agt	558
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Phe Ser	
125 130 135	
caa cct gaa ata gta cca att tct aat ata aca gaa aat gtg tac ata	606
Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val Tyr Ile	
140 145 150	
aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct aag aag atg	654
Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys Lys Met	
155 160 165	
agt gtt ttg cta aga acc aag aat tca act atc gag tat gat ggt att	702
Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp Gly Ile	
170 175 180 185	
atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac gtt tcc atc	750
Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val Ser Ile	
190 195 200	
agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg acc atc ttc	798
Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr Ile Phe	
205 210 215	
tgt att ctg gaa act gac aag acg cgg ctt tta tct tca cct ttc tct	846
Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro Phe Ser	
220 225 230	
ata gag ctt gag gac cct cag cct ccc cca gac cac att cct tgg att	894
Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro Trp Ile	
235 240 245	
aca gct gta ctt cca aca gtt att ata tgt gtg atg gtt ttc tgt cta	942

Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	
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Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	
			270						275					280		
tgt gga acc aac aca atg gag agg gaa gag agt gaa cag acc aag aaa																1038
Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	
			285					290					295			
aga gaa aaa atc cat ata cct gaa aga tct gat gaa gcc cag cgt gtt																1086
Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	
		300					305					310				
ttt aaa agt tgc aag aca tct tca tgc gac aaa agt gat aca tgt ttt																1134
Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys	Phe	
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 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(96)

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1				5				10					15			
ctt acc ttc ggg cct gaa gaa gca tta gct gaa cag acc gtc ttc ctt																96
Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu	
			20					25					30			

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ctttcagcac	cgtgctagct	gatctttcgg	acaacttgac	acaagataga	gttaactggg	216
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cttttctgaa	gagaagtgg	gggagagtgg	atgggggtgg	ggcagaggaa	aagtggggga	516
gagggcctgg	gaggagagga	gggaggggga	cgggggtggg	gtggggaaaa	ctatggttgg	576
gatgtaaaaa	cggataataa	tataaatatt	aaataaaaaag	agagtattga	gca	629

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 <213> Mus musculus

<400> 26																
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			20					25					30			

<210> 27
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(69)

<400> 27
 tgc ttt gcc cca aga tgc aga gag aga agg agg aat gag aga ttg aga 48
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 agg gaa agt gta cgc cct gta taacagtgtc cgcagaagca aggggctgaa 99
 Arg Glu Ser Val Arg Pro Val
 20
 aagatctgaa ggtagcctcc gtcattctctt ctgggataca tggatcgtgg ggatcatgag 159
 gcattcttcc cttaacaaat ttaagctggt ttacccacta cctcaccttc ttaaaaacct 219
 ctttcagatt aagctgaaca gttacaagat ggctggcatc cctctccttt ctccccatat 279
 gcaatttgct taatgtaacc tcttcttttg ccatgtttcc attctgccat cttgaattgt 339
 cttgtcagcc aattcattat ctattaaaca ctaatttgag 379

<210> 28
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 28
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 Arg Glu Ser Val Arg Pro Val
 20

<210> 29
 <211> 261
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(135)

<400> 29
 cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc tct aag 48
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15
 tta gag cgg gat agt aac gct gac aga gag act atc aac ctg aag gaa 96
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30
 ctt gaa ccc caa att gct tca gca aaa cca aat gca gag tgaaggcagt 145
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45
 gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc agagttttctc 205
 agaattcaaa aatgtttctca gctgattgga attctacagt tgaataatta aagaac 261

<210> 30
 <211> 45
 <212> PRT
 <213> Mus musculus

<400> 30
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45

<210> 31
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(183)

<400> 31
 aaa tgg aag aag aag aag cgg cct cgc aac tct tat aaa tgt gga acc 48
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15
 aac aca atg gag agg gaa gag agt gaa cag acc aag aaa aga gaa aaa 96
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30
 atc cat ata cct gaa aga tct gat gaa gcc cag cgt gtt ttt aaa agt 144
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45
 tcg aag aca tct tca tgc gac aaa agt gat aca tgt ttt taattaaaga 193
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60
 gtaaagccca aaaaaaa 210

<210> 32
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 32
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60

<210> 33
 <211> 359
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(359)

<400> 33

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gagttttata cctcaataga ctcttactag tttctctttt tcaggttggt aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
tggatgccat ccaggcttct tttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
        1             5             10

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aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
  15             20             25             30

```

```

ctt tca caa gtg tct tca gat 359
Leu Ser Gln Val Ser Ser Asp
          35

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<210> 34

<211> 37

<212> PRT

<213> Mus musculus

<400> 34

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Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
  1             5             10             15
Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
          20             25             30
Gln Val Ser Ser Asp
          35

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<210> 35

<211> 416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (318)...(416)

<400> 35

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ccaaagaaaa agtgatttgt cattgcttta tagactgtaa gaagagaaca tctcagaagt 60
ggagtctttac cctgaaatca aaggatttaa agaaaaagtg gaatttttct tcagcaagct 120
gtgaaactaa atccacaacc ttggagacc caggaaacacc ctccaatctc tgtgtgtttt 180
gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcagc cctgcctgtt 240
ttgcacctgg gaagtgcctt ggtcttactt gggtcctaat tggttgcttt cacttttgac 300
cctaagcatc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
      Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
        1             5             10

```

```

tcc aag tgt cca tac ctg aat ttc ttt cag ctc ttg gtg ctg gct ggt 398
Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
          15             20             25

```

ctt tct cac ttc tgt tca
 Leu Ser His Phe Cys Ser
 30

416

<210> 36
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 Ser

<210> 37
 <211> 113
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (99)...(113)

<400> 37
 ggagcaagca gacgcgtaag agtggctcct gtaggcagca cggacttgaa caaccagact 60
 cctgtagacg tgttcagaa cttacggaag caccacag atg gac ccc aga tgc 113
 Met Asp Pro Arg Cys
 1 5

<210> 38
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 38
 Met Asp Pro Arg Cys
 1 5

<210> 39
 <211> 124
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)...(124)

<400> 39
 cacagggtga aagctttgct tctctgctgc tgtaacaggg actagcacag acacacggat 60
 gagtgggggtc atttcagat attaggtcac agcagaagca gccaaa atg gat ccc 115
 Met Asp Pro
 1

cag tgc act
Gln Cys Thr
5

124

<210> 40
<211> 6
<212> PRT
<213> Homo sapiens

<400> 40
Met Asp Pro Gln Cys Thr
1 5

<210> 41
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (148)...(195)

<400> 41
aggagcctta ggaggtacgg ggagctcgca aatactcctt ttggtttatt cttaccacct 60
tgcttctgtg ttccttggga atgctgctgt gcttatgcat ctggctctctt tttggagcta 120
cagtggacag gcatttgtga cagcaact atg gga ctg agt aac att ctc ttt gtg 174
Met Gly Leu Ser Asn Ile Leu Phe Val
1 5

atg gcc ttc ctg ctc tct ggt 195
Met Ala Phe Leu Leu Ser Gly
10 15

<210> 42
<211> 16
<212> PRT
<213> Homo sapiens

<400> 42
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15